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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/071,458

DATE: 02/28/2002

TIME: 12:41:12

Input Set : A:\EP.txt

Output Set: N:\CRF3\02282002\J071458.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company

5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL

BETA-SUBUNIT,

6 K+betaM3

8 <130> FILE REFERENCE: D0114.np

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/071,458

C--> 10 <141> CURRENT FILING DATE: 2002-02-07

10 <150> PRIOR APPLICATION NUMBER: US 60/267,039

11 <151> PRIOR FILING DATE: 2001-02-05

13 <150> PRIOR APPLICATION NUMBER: US 60/281,224

14 <151> PRIOR FILING DATE: 2001-04-03

16 <160> NUMBER OF SEQ ID NOS: 76

18 <170> SOFTWARE: PatentIn version 3.0

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 1418

22 <212> TYPE: DNA

23 <213> ORGANISM: homo sapiens

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (417)..(1097)

29 <400> SEQUENCE: 1

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32 ttgtctaaca cgtatatatt ctctgtaaag cacatcacag cctttctgca cttaggaaca 120

34 ttagacagca cttcagcagt acacttgggg gccattttaa acaattaaat cactgatagg 180

36 ctccgctccg ctcagggcgg cccagacac gggtttccca tggcagcacc acggcacgcc 240

38 cggcgcacct gctgccccga acccctggct ccagggggca atgagggggc agtgggaagg 300

40 gcaactactcc tcgggcattg cctagagaag cgagaccgtc ccgccctccc gctggccctc 360

42 cttctctccc gccgggggcc cgcgcaattc tccgccagag ggacagtcgg cctcat atg 419

43 Met

44 1

46 tta aga cct ctg atc act aga tcc cct gca tct cca ctg aac aac caa 467

47 Leu Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Asn Asn Gln

48 5 10 15

50 ggc acc cct act ccg gca caa ctc aca aaa tcc aat gcg cat gtc cac 515

51 Gly Thr Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala His Val His

52 20 25 30

54 act gat gtg ggc agc cac atg tac acc agc agc ctg gcc acc ctc acc 563

55 Thr Asp Val Gly Ser His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr

56 35 40 45

58 aaa tac cct gta tcc aga atc aga aga ctt tgt gat ggt aca gag ccc 611

59 Lys Tyr Pro Val Ser Arg Ile Arg Arg Leu Cys Asp Gly Thr Glu Pro

60 50 55 60 65

62 ata gtt ttg gac agt ctc aaa cag cac tat ttc act gac aga gat gga 659

63 Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Thr Asp Arg Asp Gly

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64          70          75          80
66 cag atg ttc aga tat atc ttg aat ttt cta cga aca tcc aaa ctc ctc      707
67 Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu Leu
68          85          90          95
70 att ctt gat gat ttc aag gac tac act ttg tta tat gaa gag gca aaa      755
71 Ile Leu Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala Lys
72          100          105          110
74 tat ttt cag ctt cag ccc atg ttg ttg gag atg gaa aga tgg aag cag      803
75 Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys Gln
76          115          120          125
78 gac aga gaa act ggt cgc ttt tca agg ccc tgt gag tgc ctt gtt tgt      851
79 Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val Cys
80 130          135          140          145
82 gtg gcc cca gac ctc aga gaa agg atc acg cta agt ggt gac aaa tcc      899
83 Val Ala Pro Asp Leu Arg Glu Arg Ile Thr Leu Ser Gly Asp Lys Ser
84          150          155          160
86 ttg gta gaa gaa gtg ttt cca gag atc ggc gat gtg atg tgc aac ttt      947
87 Leu Val Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn Phe
88          165          170          175
90 atc agt gca ggc tgg aat cat gac tcc acg cac atc gtc agg ttt cca      995
91 Ile Ser Ala Gly Trp Asn His Asp Ser Thr His Ile Val Arg Phe Pro
92          180          185          190
94 cta agt ggc tac tgt cac ctc aac tca gtc cag gtc ctc gag agg ttg      1043
95 Leu Ser Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu Arg Leu
96          195          200          205
98 cag caa aga gga ttt gaa atc gtg ggc tcc tgt agg gga gga gtg ggc      1091
99 Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Arg Gly Gly Val Gly
100 210          215          220          225
102 tca tcc tagttcagca aatacgtcct tcatagggaa ctgaggcgga tgcctctccg      1147
103 Ser Ser
106 taccctccat catctggata aagcaagagc ctctggacta aacggacata tttcttatgc      1207
108 aaaaaggaaa acacacacaaa ctaataaaca aataataaaa aagggaacatt tgtgtgcagt      1267
110 tgggacagaa aaccaagtcc tgcacctaaa attgaataaa agatgcattt atatgcaata      1327
112 gagaccacac ctgtattcat atgggaacaa ttggaatagt tcaactcaaaa aaaaaaaaaa      1387
114 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
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118 <211> LENGTH: 227
119 <212> TYPE: PRT
120 <213> ORGANISM: homo sapiens
122 <400> SEQUENCE: 2
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128 Gln Gly Thr Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala His Val
129          20          25          30
132 His Thr Asp Val Gly Ser His Met Tyr Thr Ser Ser Leu Ala Thr Leu
133          35          40          45
136 Thr Lys Tyr Pro Val Ser Arg Ile Arg Arg Leu Cys Asp Gly Thr Glu
137          50          55          60
140 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Thr Asp Arg Asp

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141 65          70          75          80
144 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
145          85          90          95
148 Leu Ile Leu Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
149          100          105          110
152 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
153          115          120          125
156 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
157          130          135          140
160 Cys Val Ala Pro Asp Leu Arg Glu Arg Ile Thr Leu Ser Gly Asp Lys
161 145          150          155          160
164 Ser Leu Val Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys Asn
165          165          170          175
168 Phe Ile Ser Ala Gly Trp Asn His Asp Ser Thr His Ile Val Arg Phe
169          180          185          190
172 Pro Leu Ser Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu Arg
173          195          200          205
176 Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Arg Gly Gly Val
177          210          215          220
180 Gly Ser Ser
181 225
184 <210> SEQ ID NO: 3
185 <211> LENGTH: 257
186 <212> TYPE: PRT
187 <213> ORGANISM: homo sapiens
189 <400> SEQUENCE: 3
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192 1          5          10          15
194 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
195          20          25          30
197 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
198          35          40          45
200 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
201          50          55          60
203 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
204 65          70          75          80
206 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
207          85          90          95
209 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
210          100          105          110
212 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
213          115          120          125
215 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
216          130          135          140
218 Val Arg Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
219 145          150          155          160
221 Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
222          165          170          175
224 Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg

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225          180          185          190
227 Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
228          195          200          205
230 Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
231          210          215          220
233 Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
234 225          230          235          240
236 Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
237          245          250          255
239 Asp
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 338
244 <212> TYPE: PRT
245 <213> ORGANISM: Drosophila melanogaster
247 <400> SEQUENCE: 4
249 Met Asp Arg Glu Arg Glu Arg Asp Val Lys Ala Leu Glu Pro Arg Asp
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252 Leu Ser Ser Thr Gly Arg Ile Tyr Ala Arg Ser Asp Ile Lys Ile Ser
253          20          25          30
255 Ser Ser Pro Thr Val Ser Pro Thr Ile Ser Asn Ser Ser Ser Pro Thr
256          35          40          45
258 Pro Thr Pro Pro Ala Ser Ser Ser Val Thr Pro Leu Gly Leu Pro Gly
259          50          55          60
261 Ala Val Ala Ala Ala Ala Ala Val Gly Gly Ala Ser Ser Ala Gly
262 65          70          75          80
264 Ala Ser Ser Tyr Leu His Gly Asn His Lys Pro Ile Thr Gly Ile Pro
265          85          90          95
267 Cys Val Ala Ala Ala Ser Arg Tyr Thr Ala Pro Val His Ile Asp Val
268          100          105          110
270 Gly Gly Thr Ile Tyr Thr Ser Ser Leu Glu Thr Leu Thr Lys Tyr Pro
271          115          120          125
273 Glu Ser Lys Leu Ala Lys Leu Phe Asn Gly Gln Ile Pro Ile Val Leu
274          130          135          140
276 Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp Gly Gly Met Phe
277 145          150          155          160
279 Arg His Ile Leu Asn Phe Met Arg Asn Ser Arg Leu Leu Ile Ala Glu
280          165          170          175
282 Asp Phe Pro Asp Leu Glu Leu Leu Leu Glu Glu Ala Arg Tyr Tyr Glu
283          180          185          190
285 Val Glu Pro Met Ile Lys Gln Leu Glu Ser Met Arg Lys Asp Arg Val
286          195          200          205
288 Arg Asn Gly Asn Tyr Leu Val Ala Pro Pro Thr Pro Pro Ala Arg His
289          210          215          220
291 Ile Lys Thr Ser Pro Arg Thr Ser Ala Ser Pro Glu Cys Asn Tyr Glu
292 225          230          235          240
294 Val Val Ala Leu His Ile Ser Pro Asp Leu Gly Glu Arg Ile Met Leu
295          245          250          255
297 Ser Ala Glu Arg Ala Leu Leu Asp Glu Leu Phe Pro Glu Ala Ser Gln
298          260          265          270

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300 Ala Thr Gln Ser Ser Arg Ser Gly Val Ser Trp Asn Gln Gly Asp Trp
301          275          280          285
303 Gly Gln Ile Ile Arg Phe Pro Leu Asn Gly Tyr Cys Lys Leu Asn Ser
304          290          295          300
306 Val Gln Val Leu Thr Arg Leu Leu Asn Ala Gly Phe Thr Ile Glu Ala
307 305          310          315          320
309 Ser Val Gly Gly Gln Gln Phe Ser Glu Tyr Leu Leu Ala Arg Arg Val
310          325          330          335
312 Pro Met
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316 <211> LENGTH: 793
317 <212> TYPE: DNA
318 <213> ORGANISM: homo sapiens
320 <400> SEQUENCE: 5
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325 tatatcttga attttctacg aacatccaaa ctctctcattc ttgatgattt caaggactac      180
327 actttgttat atgaagaggc aaaatatattt cagcttcagc ccatgtgttg gagatggaaa      240
329 gatggaagca ggacagagaa actggtcgct tttcaaggcc ctgtgagtgc cttgttgttt      300
331 gtgtggcccc agacctcaga gaaaggatca cgctaagtgg tgacaaatcc ttggtagaag      360
333 aagtgtttcc agagatcggc gatgtgatgt gcaactttat cagtgcaggc tggaatcacg      420
335 actccacgca catcgtcagg ttccactaa gtggctactg tcacctcaac tcagtccagg      480
337 tcctcgagag gttgcagcaa agaggatttg aaatcgtggg ctctgtagg ggaggagtgg      540
339 gcttgtccta gttcagcaaa tacgtccttc ataggggaact gaggcggatg ccttcccgtg      600
341 ccctccatca tctggataaa gcaagagcct ctggactaaa cggacatatt tcttatgcaa      660
343 aaaggaaaaac acacacaact aataaacaaa taataaaaaa gggacatttg tgtgcagttg      720
345 ggacagaaaa ccaagtcttg cacctaaaat tgaataaaag atgcatttat atgcaataga      780
347 gaccacacct gta                                     793
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351 <211> LENGTH: 237
352 <212> TYPE: PRT
353 <213> ORGANISM: homo sapiens
355 <400> SEQUENCE: 6
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360 Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
361          20          25          30
363 Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
364          35          40          45
366 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
367          50          55          60
369 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
370 65          70          75          80
372 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
373          85          90          95
375 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
376          100          105          110
378 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
379          115          120          125

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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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